

In the Claims

1 (currently amended). A purified polynucleotide comprising a nucleotide sequence encoding a mutant large subunit of a plant ADP-glucose pyrophosphorylase polypeptide, or a biologically-active fragment of said mutant polypeptide, wherein said mutant polypeptide comprises an amino acid mutation in the amino acid sequence of said polypeptide and wherein when said mutant polypeptide is expressed to form a mutant ADP-glucose pyrophosphorylase enzyme, said mutant enzyme, or a biologically-active fragment of said mutant enzyme, exhibits increased heat stability relative to the wild type ADP-glucose pyrophosphorylase enzyme.

Claims 2-41 (canceled)

42 (new). The polynucleotide according to claim 1, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the amino acid corresponding to position 333 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

43 (new). The polynucleotide according to claim 42, wherein said amino acid corresponding to position 333 is replaced with a phenylalanine.

44 (new). The polynucleotide according to claim 42, wherein said amino acid corresponding to position 333 is replaced with a methionine.

45 (new). The polynucleotide according to claim 1, wherein said mutant polypeptide encoded by said polynucleotide further comprises an amino acid mutation that confers increased seed weight to a plant expressing said polynucleotide.

46 (new). The polynucleotide according to claim 45, wherein said polynucleotide comprises the *Rev6* mutation.

47 (new). The polynucleotide according to claim 45, wherein said mutation comprises the insertion of at least one serine residue between amino acids corresponding to positions 494 and 495 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize.

48 (new). The polynucleotide according to claim 45, wherein said mutation comprises the insertion of the amino acid pair tyrosine:serine between amino acids corresponding to positions 494 and 495 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize.

49 (new). The polynucleotide according to claim 45, wherein said mutation comprises the insertion of the amino acid pair serine:tyrosine between amino acids corresponding to positions 495 and 496 in the amino acid sequence of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize.

50 (new). The polynucleotide according to claim 1, wherein said plant is a monocotyledonous plant.

51 (new). The polynucleotide according to claim 50, wherein said monocotyledonous plant is selected from the group consisting of rice, wheat, barley, oats, sorghum, maize, lily, and millet.

52 (new). The polynucleotide according to claim 1, wherein said plant is *Zea mays*.

53 (new). The polynucleotide according to claim 1, wherein said plant is a dicotyledonous plant.

54 (new). The polynucleotide according to claim 53, wherein said dicotyledonous plant is selected from the group consisting of pea, alfalfa, chickpea, chicory, clover, kale, lentil, soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple tree, and lettuce.

55 (new). The polynucleotide according to claim 1, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the amino acid corresponding to position 426 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a phenylalanine amino acid and the amino acid corresponding to position 177 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

56 (new). The polynucleotide according to claim 55, wherein said amino acid corresponding to position 177 is replaced with a proline.

57 (new). The polynucleotide according to claim 55, wherein said amino acid corresponding to position 177 is replaced with a valine.

58 (new). The polynucleotide according to claim 1, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the amino acid corresponding to position 324 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a lysine amino acid, and the amino acid corresponding to position 359 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a valine amino acid, and the amino acid corresponding to position 396 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

59 (new). The polynucleotide according to claim 58, wherein said amino acid corresponding to position 396 is replaced with a valine.

60 (new). A method for increasing resistance of a plant to heat stress conditions, said method comprising incorporating the polynucleotide of claim 1 into the genome of said plant and expressing the protein encoded by said polynucleotide molecule.

61 (new). The method according to claim 60, wherein said plant is a monocotyledonous plant.

62 (new). The method according to claim 61, wherein said monocotyledonous plant is selected from the group consisting of rice, wheat, barley, oats, sorghum, maize, lily, and millet.

63 (new). The method according to claim 60, wherein said plant is *Zea mays*.

64 (new). The method according to claim 60, wherein said plant is a dicotyledonous plant.

65 (new). The method according to claim 64, wherein said dicotyledonous plant is selected from the group consisting of pea, alfalfa, chickpea, chicory, clover, kale, lentil, soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple tree, and lettuce.

66 (new). The method according to claim 60, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the amino acid corresponding to position 426 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a phenylalanine amino acid and the amino acid corresponding to position 177 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

67 (new). The method according to claim 66, wherein said amino acid corresponding to position 177 is replaced with a proline.

68 (new). The method according to claim 66, wherein said acid corresponding to position 177 is replaced with a valine.

69 (new). The method according to claim 60, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the amino acid corresponding to position 324 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a lysine amino acid, and the amino acid corresponding to position 359 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a valine amino acid, and the amino acid corresponding to position 396 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

70 (new). The method according to claim 69, wherein said amino acid corresponding to position 396 is replaced with a valine.

71 (new). The method according to claim 60, wherein said mutant polypeptide encoded by said polynucleotide further comprises an amino acid mutation that confers increased seed weight to a plant expressing said polynucleotide.

72 (new). A plant or plant tissue comprising the polynucleotide molecule of claim 1.

73 (new). The plant or plant tissue according to claim 72, wherein said plant or plant tissue is monocotyledonous.

74 (new). The plant or plant tissue according to claim 73, wherein said monocotyledonous plant or plant tissue is selected from the group consisting of rice, wheat, barley, oats, sorghum, maize, lily, and millet.

75 (new). The plant or plant tissue according to claim 72, wherein said plant is *Zea mays* or said plant tissue is from *Zea mays*.

76 (new). The plant or plant tissue according to claim 72, wherein said plant or plant tissue is dicotyledonous.

77 (new). The plant or plant tissue according to claim 76, wherein said dicotyledonous plant or plant tissue is selected from the group consisting of pea, alfalfa, chickpea, chicory, clover, kale, lentil, soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple tree, and lettuce.

78 (new). The plant tissue according to claim 72, wherein said plant tissue is a seed.

79 (new). The plant or plant tissue according to claim 72, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the amino acid corresponding to position 426 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a phenylalanine amino acid and the amino acid corresponding to position 177 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

80 (new). The plant or plant tissue according to claim 79, wherein said amino acid corresponding to position 177 is replaced with a proline.

81 (new). The plant or plant tissue according to claim 79, wherein said amino acid corresponding to position 177 is replaced with a valine.

82 (new). The plant or plant tissue according to claim 72, wherein said mutant polypeptide encoded by said polynucleotide comprises an amino acid mutation wherein the amino acid corresponding to position 324 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a lysine amino acid, and the amino acid corresponding to

position 359 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by a valine amino acid, and the amino acid corresponding to position 396 of the wild type large subunit of ADP-glucose pyrophosphorylase polypeptide of maize is replaced by an amino acid that confers said increased heat stability on said mutant enzyme.

83 (new). The plant or plant tissue according to claim 82, wherein said amino acid corresponding to position 396 is replaced with a valine.

84 (new). The plant or plant tissue according to claim 72, wherein said mutant polypeptide encoded by said polynucleotide further comprises an amino acid mutation that confers increased seed weight to a plant expressing said polynucleotide.